

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|------|----------|-----------------|-------------|
| ----- | ---- | ----- | ----- | ----- |
| US 6274138 | B1 | 20010814 | US 1997-922957 | 19970903 |
| US 2002086006 | A1 | 20020704 | US 2001-915694 | 20010725 |
| PRIORITY APPLN. INFO.: | | | US 1997-922957 | A3 19970903 |

AB This invention relates to nucleic acid and amino acid sequences of a human mitochondrial malate dehydrogenase (MT-MDH). Nucleic acids encoding the MT-MDH of the present invention were first identified in Incyte Clone 11587 from the human peripheral promonocyte cell line cDNA library (THP1PLB01) using a computer search for amino acid sequence alignments. MT-MDH is 294 amino acids in length and has chemical and structural homol. with murine mitochondrial malate dehydrogenase and porcine mitochondrial malate dehydrogenase. Northern anal. shows the expression of this sequence in various libraries. The invention also provides expression vectors, host cells, agonists, antibodies and antagonists. The invention also provides methods for treating disorders associated with expression of MT-MDH.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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| NEWS 1 | | Web Page for STN Seminar Schedule - N. America |
| NEWS 2 | JUL 02 | LMEDLINE coverage updated |
| NEWS 3 | JUL 02 | SCISEARCH enhanced with complete author names |
| NEWS 4 | JUL 02 | CHEMCATS accession numbers revised |
| NEWS 5 | JUL 02 | CA/CAPplus enhanced with utility model patents from China |
| NEWS 6 | JUL 16 | CAPplus enhanced with French and German abstracts |
| NEWS 7 | JUL 18 | CA/CAPplus patent coverage enhanced |
| NEWS 8 | JUL 26 | USPATFULL/USPAT2 enhanced with IPC reclassification |
| NEWS 9 | JUL 30 | USGENE now available on STN |
| NEWS 10 | AUG 06 | CAS REGISTRY enhanced with new experimental property tags |
| NEWS 11 | AUG 06 | BEILSTEIN updated with new compounds |
| NEWS 12 | AUG 06 | FSTA enhanced with new thesaurus edition |
| NEWS 13 | AUG 13 | CA/CAPplus enhanced with additional kind codes for granted patents |
| NEWS 14 | AUG 20 | CA/CAPplus enhanced with CAS indexing in pre-1907 records |
| NEWS 15 | AUG 27 | Full-text patent databases enhanced with predefined patent family display formats from INPADOCDB |
| NEWS 16 | AUG 27 | USPATOLD now available on STN |
| NEWS 17 | AUG 28 | CAS REGISTRY enhanced with additional experimental spectral property data |
| NEWS 18 | SEP 07 | STN AnaVist, Version 2.0, now available with Derwent World Patents Index |
| NEWS 19 | SEP 13 | FORIS renamed to SOFIS |
| NEWS 20 | SEP 13 | INPADOCDB enhanced with monthly SDI frequency |
| NEWS 21 | SEP 17 | CA/CAPplus enhanced with printed CA page images from |

1967-1998

NEWS 22 SEP 17 CAplus coverage extended to include traditional medicine patents

NEWS 23 SEP 24 EMBASE, EMBAL, and LEMBASE reloaded with enhancements

NEWS 24 OCT 02 CA/CAplus enhanced with pre-1907 records from Chemisches Zentralblatt

NEWS EXPRESS 19 SEPTEMBER 2007: CURRENT WINDOWS VERSION IS V8.2, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 SEPTEMBER 2007.

NEWS HOURS STN Operating Hours Plus Help Desk Availability

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NEWS IPC8 For general information regarding STN implementation of IPC 8

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* * * * * STN Columbus * * * * *

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=> file reg

| | | |
|----------------------|------------------|---------------|
| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
| FULL ESTIMATED COST | 0.21 | 0.21 |

FILE 'REGISTRY' ENTERED AT 07:57:31 ON 16 OCT 2007

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STRUCTURE FILE UPDATES: 15 OCT 2007 HIGHEST RN 950725-14-1

DICTIONARY FILE UPDATES: 15 OCT 2007 HIGHEST RN 950725-14-1

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=> s

KAKAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGIEKNLGIGKVSSFEEKMISDAIPE
LKASIKKGEDFVKTLK/sqep

2 KAKAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGIEKN
LGIGKVSSFEEKMISDAIPELKASIKKGEDFVKTLK/SQEP

68052 SQL=100

L1 2 KAKAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGIEKN
LGIGKVSSFEEKMISDAIPELKASIKKGEDFVKTLK/SQEP
(KAKAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETECTYFSTPLLLGKKGI
EKNLGIGKVSSFEEKMISDAIPELKASIKKGEDFVKTLK/SQEP AND SQL=100)

=> file caplus

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

7.70

7.91

FILE 'CAPLUS' ENTERED AT 07:57:45 ON 16 OCT 2007

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FILE COVERS 1907 - 16 Oct 2007 VOL 147 ISS 17

FILE LAST UPDATED: 15 Oct 2007 (20071015/ED)

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=> s l1

L2 2 L1

=> d ibib 1-2

L2 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2004:681680 CAPLUS

DOCUMENT NUMBER: 141:200162

TITLE: Mitochondrial malate dehydrogenase DNA fragmentation activator fragment and related conjugated proteins and antibodies for cancer therapy

INVENTOR(S): Wright, Susan C.; Larrick, James W.; Nock, Steffen R.; Wilson, David S.

PATENT ASSIGNEE(S): Palo Alto Institute of Molecular Medicine, USA

SOURCE: PCT Int. Appl., 225 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|------|----------|-----------------|----------|
| WO 2004070012 | A2 | 20040819 | WO 2004-US2974 | 20040202 |
| WO 2004070012 | A3 | 20060330 | | |

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
 BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU,
 MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN,
 GQ, GW, ML, MR, NE, SN, TD, TG, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
 AU 2004209644 A1 20040819 AU 2004-209644 20040202
 CA 2514841 A1 20040819 CA 2004-2514841 20040202
 US 2004191843 A1 20040930 US 2004-770668 20040202
 EP 1590440 A2 20051102 EP 2004-707424 20040202
 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
 IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK
 JP 2006522021 T 20060928 JP 2006-503266 20040202
 PRIORITY APPLN. INFO.: US 2003-444191P P 20030203
 US 2003-460855P P 20030408
 US 2004-770668 A 20040202
 WO 2004-US2974 W 20040202

L2 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2007 ACS on STN
 ACCESSION NUMBER: 2004:681539 CAPLUS
 DOCUMENT NUMBER: 141:212819
 TITLE: Compounds useful in coating stents to prevent and
 treat stenosis and restenosis
 INVENTOR(S): Wang, Yuqiang; Larrick, James W.; Wright, Susan C.
 PATENT ASSIGNEE(S): Medlogics Device Corporation, USA
 SOURCE: PCT Int. Appl., 63 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|-------------------|-----------------|------------|
| WO 2004069201 | A2 | 20040819 | WO 2004-US3143 | 20040203 |
| WO 2004069201 | A3 | 20050519 | | |
| W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG | | | | |
| US 2007037739 | A1 | 20070215 | US 2006-544241 | 20060103 |
| PRIORITY APPLN. INFO.: | | | US 2003-444391P | P 20030203 |
| | | | WO 2004-US3143 | W 20040203 |
| OTHER SOURCE(S): | | MARPAT 141:212819 | | |

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| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
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| FULL ESTIMATED COST | 3.77 | 11.68 |

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| NEWS | 5 | JUL 02 | CA/CAPplus enhanced with utility model patents from China |
| NEWS | 6 | JUL 16 | Caplus enhanced with French and German abstracts |
| NEWS | 7 | JUL 18 | CA/CAPplus patent coverage enhanced |
| NEWS | 8 | JUL 26 | USPATFULL/USPAT2 enhanced with IPC reclassification |
| NEWS | 9 | JUL 30 | USGENE now available on STN |
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| NEWS | 19 | SEP 13 | FORIS renamed to SOFIS |
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| NEWS | 21 | SEP 17 | CA/CAPplus enhanced with printed CA page images from 1967-1998 |
| NEWS | 22 | SEP 17 | Caplus coverage extended to include traditional medicine patents |
| NEWS | 23 | SEP 24 | EMBASE, EMBAL, and LEMBASE reloaded with enhancements |
| NEWS | 24 | OCT 02 | CA/CAPplus enhanced with pre-1907 records from Chemisches Zentralblatt |
| | | | |
| NEWS EXPRESS | 19 | SEPTEMBER 2007: CURRENT WINDOWS VERSION IS V8.2, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 19 SEPTEMBER 2007. | |
| | | | |
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| COST IN U.S. DOLLARS | SINCE FILE | TOTAL |
| | ENTRY | SESSION |
| FULL ESTIMATED COST | 0.42 | 0.42 |

FILE 'PCTFULL' ENTERED AT 08:01:14 ON 16 OCT 2007
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| FILE LAST UPDATED: | 16 OCT 2007 | <20071016/UP> |
| MOST RECENT UPDATE WEEK: | 200741 | <200741/EW> |
| FILE COVERS 1978 TO DATE | | |

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=> s WO0166689/pn
L1 0 WO0166689/PN
(WO166689/PN)

=> s WO 0166689/pn
L2 0 WO 0166689/PN
(WO166689/PN)

=> s WO200166689/pn
L3 1 WO200166689/PN
(WO2001066689/PN)

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| | | | |
|---------------------|---------------|---|---------------------------------|
| L3 | ANSWER 1 OF 1 | PCTFULL | COPYRIGHT 2007 Univentio on STN |
| ACCESSION NUMBER: | | 2001066689 | PCTFULL ED 20020822 |
| TITLE (ENGLISH): | | NOVEL NUCLEIC ACIDS AND POLYPEPTIDES | |
| TITLE (FRENCH): | | NOUVEAUX ACIDES NUCLEIQUES ET POLYPEPTIDES | |
| INVENTOR(S): | | TANG, Y., Tom; LIU, Chenghua; ASUNDI, Vinod; XU, Chongjun; WEHRMAN, Tom; REN, Feiyan; MA, Yunqing; ZHOU, Ping; ZHAO, Qing, A.; YANG, Yonghong; DRMANAC, Radoje, T.; ZHANG, Jie; CHEN, Rui-hong; XUE, Aidong, J.; WANG, Jian-Rui | |
| PATENT ASSIGNEE(S): | | HYSEQ, INC.; TANG, Y., Tom; LIU, Chenghua; ASUNDI, Vinod; XU, Chongjun; WEHRMAN, Tom; REN, Feiyan; MA, Yunqing; | |

ZHOU, Ping;
ZHAO, Qing, A.;
YANG, Yonghong;
DRMANAC, Radoje, T.;
ZHANG, Jie;
CHEN, Rui-hong;
XUE, Aidong, J.;
WANG, Jian-Rui
Patent

DOCUMENT TYPE:
PATENT INFORMATION:

| NUMBER | KIND | DATE |
|---------------|------|----------|
| WO 2001066689 | A2 | 20010913 |

DESIGNATED STATES
W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF
CG CI CM GA GN GW ML MR NE SN TD TG

PRIORITY INFO.:

US 2000-09/519,705 20000307
US 2000-09/574,454 20000519
US 2000-09/596,193 20000617
US 2000-09/616,847 20000714
US 2000-09/665,363 20000919
US 2000-09/693,267 20001020

APPLICATION INFO.:

WO 2001-US4942 A 20010305

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(FILE 'HOME' ENTERED AT 07:59:55 ON 16 OCT 2007)

FILE 'PCTFULL' ENTERED AT 08:01:14 ON 16 OCT 2007

L1 0 S WO0166689/PN
L2 0 S WO 0166689/PN
L3 1 S WO200166689/PN

=> s l3 and fragment?

142984 FRAGMENT?

L4 1 L3 AND FRAGMENT?

=> d ibib kwic

L4 ANSWER 1 OF 1 PCTFULL COPYRIGHT 2007 Univentio on STN
ACCESSION NUMBER: 2001066689 PCTFULL ED 20020822
TITLE (ENGLISH): NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE (FRENCH): NOUVEAUX ACIDES NUCLEIQUES ET POLYPEPTIDES
INVENTOR(S): TANG, Y., Tom;
LIU, Chenghua;
ASUNDI, Vinod;
XU, Chongjun;
WEHRMAN, Tom;
REN, Feiyan;
MA, Yungqing;
ZHOU, Ping;
ZHAO, Qing, A.;
YANG, Yonghong;
DRMANAC, Radoje, T.;
ZHANG, Jie;
CHEN, Rui-hong;
XUE, Aidong, J.;
WANG, Jian-Rui

PATENT ASSIGNEE(S): HYSEQ, INC.;
TANG, Y., Tom;
LIU, Chenghua;
ASUNDI, Vinod;
XU, Chongjun;
WEHRMAN, Tom;
REN, Feiyan;
MA, Yunqing;
ZHOU, Ping;
ZHAO, Qing, A.;
YANG, Yonghong;
DRMANAC, Radoje, T.;
ZHANG, Jie;
CHEN, Rui-hong;
XUE, Aidong, J.;
WANG, Jian-Rui
DOCUMENT TYPE: Patent

PATENT INFORMATION:

| NUMBER | KIND | DATE |
|---------------|------|----------|
| WO 2001066689 | A2 | 20010913 |

DESIGNATED STATES

W:

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
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TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF
CG CI CM GA GN GW ML MR NE SN TD TG

PRIORITY INFO.:

US 2000-09/519,705 20000307
US 2000-09/574,454 20000519
US 2000-09/596,193 20000617
US 2000-09/616,847 20000714
US 2000-09/665,363 20000919
US 2000-09/693,267 20001020

APPLICATION INFO.:

WO 2001-US4942 A 20010305

PI WO 2001066689

A2 20010913

DETD . . . at least 90% identity to an identifying
sequence of SEQ ID NO: 1-1 88, or 377-564 or a degenerate variant or
fragment thereof. The
identifying sequence can be 1 00 base pairs in length.

The term expression modulating fragment, EMF, means a series
of nucleotides which
modulates the expression of an operably linked ORF or another EMF.

EMF. EMFs

include, but are not limited to, promoters, and promoter modulating
sequences (inducible
elements). One class of EMFs are nucleic acid fragments which
induce the expression of an
operably linked ORF in response to a specific regulatory factor or
physiological event.

in the sequences

provided herein is substituted with U (uracil). Generally, nucleic acid
segments provided by this
invention may be assembled from fragments of the genome and
short oligonucleotide linkers, or
from a series of oligonucleotides, or from individual nucleotides, to
provide a synthetic. . .

The tenns oligonucleotide fragment or a polynucleotide

fragment, portion, or
segment or probe or primer are used interchangeably and refer to a
sequence of nucleotide
residues which are at least. . . least about 9 nucleotides, more
preferably at least about 11 nucleotides and
most preferably at least about 17 nucleotides. The fragment is
preferably less than about 500
nucleotides, preferably less than about 200 nucleotides, more preferably
less than about 100
nucleotides, more. . . 50 nucleotides, more preferably from about 17
to 30

7
nucleotides and most preferably from about 20 to 25 nucleotides.
Preferably the fragments can
be used in polymerase chain reaction (PCR), various hybridization
procedures or microarray
procedures to identify or amplify identical or related parts of mRNA or
DNA molecules. A
fragment or segment may uniquely identify each polynucleotide
sequence of the present
invention. Preferably the fragment comprises a sequence
substantially similar to any one of SEQ
ID NOs - 1-188, or 377
Probes may, . . .

The terms polypeptide or peptide or amino acid sequence refer to an
oligopeptide,
peptide, polypeptide or protein sequence or fragment thereof
and to naturally occurring or
synthetic molecules. A polypeptide fragment, portion, or
segment is a stretch of amino
acid residues of at least about 5 amino acids, preferably at least.
. . .

10 As used herein, an uptake modulating fragment, UMF, means
a series of nucleotides
which mediate the uptake of a linked DNA fragment into a cell.
UMFs can be readily identified
using known UMFs as a target sequence or target motif with the
computer-based. . .

. . .
obtained from one or more public databases, such as
dbEST, gbpri, and UniGene. The EST sequences can provide identifying
sequence information,
representative fragment or segment information, or novel
segment information for the full-length
gene.

Included within the scope of the nucleic acid sequences of the invention
are nucleic acid
sequence fragments that hybridize under stringent conditions
to any of the nucleotide sequences
of SEQ ID NO: 1-188, or 377-564, or complements thereof, which
fragment is greater than about
15
nucleotides, preferably 7 nucleotides, more preferably greater than 9
nucleotides and most
preferably greater than 17 nucleotides. Fragments of, e.g. 15,
17, or 20 nucleotides or more that
are selective for (i.e. specifically hybridize to any one of the. . .

. . .
0 variations can be routinely determined by comparing the
sequence provided in SEQ ID NO: 1-188,
or 377-564, a representative fragment thereof, or a
nucleotide sequence at least 90% identical,

preferably 95% identical, to SEQ ID NO: I- 1 8 8, or. . .

. . .
region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this 3 0 gives a polynucleotide encoding the desired amino acid variant.

. . .
constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-1 88, or '377-564 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such. . . into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-1 88, or 377-564 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the. . .

. . .
complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: I- IS 8, or 3 77-564, or fragments, analogs or derivatives thereof. An antisense nucleic acid comprises a nucleotide sequence that is complementary to a sense nucleic acid encoding a. . . 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of 20
SEQ ID NO: 189-376, or 565-752 or antisense nucleic acids complementary.

. . .
one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

. . .
variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO: 189-3 76, or 5 65

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in. . .

Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such

fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention further provides isolated polypeptides encoded by the nucleic acid

fragments of the present invention or by degenerate variants of the nucleic acid fragments of the

present invention. By degenerate variant is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes. . .

and
Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

29
retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

p
Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and. . .

is defined in accordance with the present invention as an isolated protein.

31
The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini. . .

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS. . .

gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants)] including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or

I 0 indirectly activate or inhibit the polypeptides of. . .

screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

4 13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques.

The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface. . . of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

55

transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which. . .

DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides. . .

In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the. . .

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety. . .

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term antibody as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig). . . binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab, Fab', and F(ab')₂ fragments, and an Fab expression library. In general, an

antibody molecule obtained from
humans relates to any of the classes IgG, IgM, . . .

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as the amino. . . such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, . . .

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

. . .
be used for the production of polyclonal or 10 monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor. . .

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen. . .

. . .
without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence. . .

. . .
selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication 4 5 Fab FRAGMENTS AND SINGLE CHAIN ANTIBODIES
According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic. . .

. . .
Fab expression libraries (see e.g.,

Huse, et al., 1989 Science 246: 1275-128 1) to allow rapid and effective identification of monoclonal Fab fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F(ab')₂

fragment produced by pepsin digestion of an antibody molecule;
(ii) an Fab fragment generated by reducing the disulfide bridges of an F(ab')₂ fragment;
(iii) an Fab fragment generated by the treatment of the antibody molecule with papain and a reducing agent and
(iv) F₂ fragments.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g.

F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody

fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These

5 fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

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stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments

generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB

derivatives is then reconverted to the Fab'-thiol by reduction with. . .

Additionally, Fab' fragments can be directly recovered from E. coli and chemically

coupled to form bispecific antibodies. Shalaby et al., J. ENP. Med. 175:217-225 (1992) describe

the production of a fully humanized bispecific antibody F(ab')₂ molecule, Each Fab' fragment

I 0 was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The. . .

Various techniques for making and isolating bispecific antibody fragments directly from

5 recombinant cell culture have also been described. For example, bispecific antibodies have been

produced using leucine zippers. Kostelny et. . . technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6449 (1993) has provided an

alternative mechanism for making bispecific antibody fragments . The fragments comprise a

heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker

which is too short to allow pairing between the two domains on the same chain. Accordingly,

the VIj and VL domains of one fragment are forced to pair with the complementary VL and VH

domains of another fragment, thereby forming two antigen-binding sites. Another strategy for

making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been

reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

a
cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a ³²S radioconjugate).

J,
Chemotherapeutic agents useful in the generation of such immunconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, . . .

By providing any of the nucleotide sequences SEQ ID NO: I- 1 8 8, or 3 77-564 or a representative fragment thereof, or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO: 1-188, or. . . a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of.

. . .
sequence or target structural motif with the sequence information stored within the data storage means. . Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif A variety of known algorithms are. . . acids, more preferably from about 10 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or. . .

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or. . .

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described. . .

to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to 'sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic.

leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI*), yield a quasi-random distribution of DNA fragments from the small molecule pUC 19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI* digest of pUC 19 that was size fractionated by a rapid gel filtration method and. . . and 10 PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

repair, chemical extraction, or agarose gel 15 electrophoresis and elution are needed. Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved. . . DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the. . .

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---Logging off of STN---

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Executing the logoff script...

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| COST IN U.S. DOLLARS | SINCE FILE | TOTAL |
| | ENTRY | SESSION |
| FULL ESTIMATED COST | 18.69 | 19.11 |

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